

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 21, 2005, 13:41:21 ; Search time 39 Seconds  
(without alignments)  
268.914 Million cell updates/sec

Title: US-10-700-314-2  
Perfect score: 109  
Sequence: 1 MKF1STSLMLLVSSLPV.....VLKRSSSTLPVPVFKRKIP 109

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 6

Total number of hits satisfying chosen parameters: 529

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR\_79:.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	9	8.3	1139	2 A49370	E1A-associated cyc
2	8	7.3	102	2 T36017	probable SecG-like
3	7	6.4	90	2 F82571	hypothetical prote
4	7	6.4	94	2 T03751	hypothetical prote
5	7	6.4	174	2 T08702	hypothetical prote
6	7	6.4	235	2 A99603	hypothetical prote
7	7	6.4	312	2 H70107	methionyl-tRNA for
8	7	6.4	331	2 A81118	dihydroxyacetone k
9	7	6.4	331	2 AG1478	dihydroxyacetone k
10	7	6.4	398	2 A45633	rhoxy-associat
11	7	6.4	427	2 F64084	3-Deoxy-manno-octu
12	7	6.4	496	2 C64935	hypothetical prote
13	7	6.4	496	2 E90936	probable transport
14	7	6.4	496	2 A85785	probable transport
15	7	6.4	521	2 E95052	hypothetical prote
16	7	6.4	570	2 S70400	zona pellucida gly
17	7	6.4	608	2 B70188	hypothetical prote
18	7	6.4	722	2 S64492	hypothetical prote
19	7	6.4	738	2 E95952	probable membrane
20	7	6.4	837	2 T19271	hypothetical prote
21	7	6.4	958	2 T44046	hypothetical prote
22	7	6.4	1227	2 A86245	hypothetical prote
23	7	6.4	1378	1 I48751	protein-tyrosine k
24	7	6.4	2948	2 T22664	hypothetical prote
25	6	5.5	40	2 H95063	hypothetical prote
26	6	5.5	57	1 SHNZE2	small hydrophobic
27	6	5.5	57	1 SHNZE4	small hydrophobic
28	6	5.5	65	2 S08014	calcium-binding pr
29	6	5.5	69	2 G82496	hypothetical prote

transforming growt  
hypothetical prote  
NADH2 dehydrogenas  
sperm-specific pro  
peptide YY precurs  
conserved hypothet  
very hypothetical  
sperm-specific pro  
hypothetical prote  
hypothetical prote  
conserved hypothet  
hypothetical prote  
hypothetical prote  
hypothetical prote  
mating pheromone a

ALIGNMENTS

RESULT 1

A49370

E1A-associated cyclin-binding protein p130 - human

N:Alternate names: adenovirus E1A-associated 130K protein; retinoblastoma-like protein 2

C:Species: Homo sapiens (man)

C:Date: 07-Apr-1994 #sequence revision 18-Nov-1994 #text\_change 09-Jul-2004

C:Accession: A49370; A49369; I38150; S36648

R:Hannon, G.J.; Demetrick, D.; Beach, D.

Genes Dev. 7, 2378-2391, 1993

A:Title: Isolation of the Rb-related p130 through its interaction with CDK2 and cyclins.

A:Reference number: A49370; MUID:94074896; PMID:8253384

A:Accession: A49370

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-1139 <HAN>

A:Cross-references: UNIPROT:Q08999; GB:S67171; NID:G453131; PIDN:AAB29227.1; PID:G453132

A:Experimental source: HeLa S3 suspension cells

A>Note: sequence extracted from NCBI backbone (NCBIN:140576, NCBIP:140577)

R:Li, Y.; Graham, C.; Lacy, S.; Duncan, A.M.V.; Whyte, P.

Genes Dev. 7, 2366-2377, 1993

A:Title: The adenovirus E1A-associated 130-kD protein is encoded by a member of the ret

A:Reference number: A49369; MUID:94074895; PMID:8253383

A:Accession: A49369

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-36, 'S', '38-63, 'P', '65-658, 'RL', '661-1139 <LIA>

A:Cross-references: GB:X76061

R:Mayol, X.; Grana, X.; Baldi, A.; Sang, N.; Hu, Q.; Giordano, A.

Oncogene 8, 2561-2566, 1993

A:Title: Cloning of a new member of the retinoblastoma gene family (pRb2) which binds to

A:Reference number: I38150; MUID:93368960; PMID:8361765

A:Accession: I38150

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 58-205, 'M', '207-1139 <MAY>

A:Cross-references: EMBL:X74594; NID:G397147; PIDN:CAA52671.1; PID:G397148

C:Genetics:

A:Gene: GDB:RBL2

A:Cross-references: GDB:269890; OMIM:180203

A:Map position: 16q12.2-16q12.2

C:Superfamily: retinoblastoma-associated protein

C:Keywords: cell cycle control

Query Match 8.3%; Score 9; DB 2; Length 1139;

Best Local Similarity 100.0%; Pred. No. 0.55;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 94 RSSSTLPVP 102

|||||

Db 970 RSSSTLPVP 978

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RESULT 2
T36017
Probable secG-like integral membrane protein - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T36017
R;Seeger, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, March 1999
A;Reference number: Z21581
A;Accession: T36017
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-102 <SE>
A;Cross-references: UNIPROT:Q92521; EMBL:AL035591; PIDN:CAB38134.1; GSPDB:GN00070; SCORE
A;Experimental source: strain A3(2)
C;Genetics:
A;Gene: SCOEDB:SCC54.04C

Query Match          7.3%; Score 8; DB 2; Length 102;
Best Local Similarity 100.0%; Pred. No. 0.76;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  7 SLILMLIV 14
    |||||
DB  37 SLILMLIV 44

RESULT 3
F82571
hypothetical protein XF2321 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: F82571
R;anonymus, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: F82571
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-90 <STM>
A;Cross-references: UNIPROT:Q9PB24; GB:AE004043; GB:AE003849; NID:g9107486; PIDN:AAF8512
A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H
as-Neto, E.; Docena, C.; El-Dorfy, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuranae, E.E.; Laig
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A;Reference number: A59328
A;Contents: annotation
C;Genetics:
A;Gene: XF2321

Query Match          6.4%; Score 7; DB 2; Length 90;
Best Local Similarity 100.0%; Pred. No. 7.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  5 STSLML 11
    |||||
DB  62 STSLML 68

RESULT 4
T03751
hypothetical protein A - slime mold (Physarum polycephalum) mitochondrion integrated pla

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C;Species: mitochondrion Physarum polycephalum
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: T03751
R;Nakagawa, C.C.; Jones, E.P.; Miller, D.L.
Curr. Genet. 33, 178-187, 1998
A;Title: Mitochondrial DNA rearrangements associated with mF plasmid integration and pla
A;Reference number: Z15055; MUID:98177147; PMID:9508792
A;Accession: T03751
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-94 <NAK>
A;Cross-references: UNIPROT:O20627; EMBL:AF012249; NID:g2435419; PIDN:AAC15931.1; PID:g2
A;Experimental source: strain aux2-S
C;Genetics:
A;Genome: mitochondrion integrated plasmid mF
C;Keywords: mitochondrion

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Query Match          6.4%; Score 7; DB 2; Length 94;
Best Local Similarity 100.0%; Pred. No. 7.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  4 ISTSLLL 10
    |||||
DB  25 ISTSLLL 31

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RESULT 5
T08702
hypothetical protein DKFP564O243.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: T08702
R;Wambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, March 1999
A;Reference number: Z16471
A;Accession: T08702
A;Molecule type: mRNA
A;Residues: 1-174 <WAM>
A;Cross-references: UNIPROT:Q9Y3T7; EMBL:AL050015
A;Experimental source: fetal brain; clone DKFP564O243
C;Genetics:
A;Note: DKFP564O243.1

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Query Match          6.4%; Score 7; DB 2; Length 174;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY  7 SLILMLL 13
    |||||
DB  48 SLILMLL 54

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RESULT 6
A93603
hypothetical protein MYPV 7290 [imported] - Mycoplasma pulmonis (strain UAB CTIP)
C;Species: Mycoplasma pulmonis
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C;Accession: A93603
R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;
Nucleic Acids Res. 29, 2145-2153, 2001
A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm
A;Reference number: A93512; MUID:21267165; PMID:11353084
A;Accession: A93603
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-235 <KUR>
A;Cross-references: UNIPROT:Q98PU3; GB:AL445566; PID:g14090144; PIDN:CAC13902.1; GSPDB:GN
A;Experimental source: strain UAB CTIP
C;Genetics:
A;Gene: MYPV_7290
A;Genetic code: SGC3

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Query Match          6.4%; Score 7; DB 2; Length 235;

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Best Local Similarity 100.0%; Pred. No. 18;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 FISTSL 9  
|||||  
Db 12 FISTSL 18

RESULT 7  
H70107  
methionyl-tRNA formyltransferase (EC 2.1.1.2.9) - Lyme disease spirochete  
C:Species: Borrelia burgdorferi (Lyme disease spirochete)  
C:Date: 13-Feb-1998 #sequence\_revision 13-Feb-1998 #text\_change 09-Jul-2004  
C:Accession: H70107  
R:Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White  
son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,  
Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.  
Nature 390, 580-586, 1997  
A:Authors: Smith, H.O.; Venter, J.C.  
A:Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.  
A:Reference number: A70100; MUID:98065943; PMID:9403685  
A:Accession: H70107  
A>Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-312 <KLE>  
A:Cross-references: UNIPROT:O51091; GB:AE001119; GB:AE000783; NID:g2687936; PIDN:AAC6644  
A:Experimental source: strain B31  
C:Superfamily: methionyl-tRNA formyltransferase; phosphoribosylglycinamide formyltransferase  
C:Keywords: protein biosynthesis; transferase

Query Match 6.4%; Score 7; DB 2; Length 312;  
Best Local Similarity 100.0%; Pred. No. 23;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 LVSSLS 19  
|||||  
Db 165 LVSSLS 171

RESULT 8  
AB1118  
dihydroxyacetone kinase homolog lmo0348 [imported] - Listeria monocytogenes (strain EGD-  
C:Species: Listeria monocytogenes  
C:Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 09-Jul-2004  
C:Accession: AE1118  
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker  
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.  
D.; Jones, L.M.; Karst, U.  
Science 294, 849-852, 2001  
A:Authors: Kref, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma  
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,  
A:Title: Comparative genomics of Listeria species.  
A:Reference number: AB1077; MUID:21537279; PMID:11679669  
A:Accession: AE1118  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-331 <GLA>  
A:Cross-references: UNIPROT:Q8YA18; GB:NC\_003210; PIDN:CAC98427.1; PID:gl6409726; GSPDB:  
A:Experimental source: strain EGD-e  
C:Genetics:  
A:Gene: lmo0348

Query Match 6.4%; Score 7; DB 2; Length 331;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 95 SSSTLP 101  
|||||  
Db 192 SSSTLP 198

RESULT 9  
AG1478

dihydroxyacetone kinase homolog lin0366 [imported] - Listeria innocua (strain Clip11262)  
C:Species: Listeria innocua  
C:Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 09-Jul-2004  
C:Accession: AG1478  
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker  
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.  
D.; Jones, L.M.; Karst, U.  
Science 294, 849-852, 2001  
A:Authors: Kref, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma  
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,  
A:Title: Comparative genomics of Listeria species.  
A:Reference number: AB1077; MUID:21537279; PMID:11679669  
A:Accession: AG1478  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-331 <GLA>  
A:Cross-references: UNIPROT:Q92HU2; GB:AL592022; PIDN:CAC95599.1; PID:gl6412795; GSPDB:G  
A:Experimental source: strain Clip11262  
C:Genetics:  
A:Gene: lin0366

Query Match 6.4%; Score 7; DB 2; Length 331;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 95 SSSTLP 101  
|||||  
Db 192 SSSTLP 198

RESULT 10  
A45633  
rhoptry-associated protein 2 - malaria parasite (Plasmodium falciparum)  
C:Species: Plasmodium falciparum  
C:Date: 22-Apr-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
C:Accession: A45633  
R:Saul, A.; Cooper, J.; Hauguitz, D.; Irving, D.; Cheng, Q.; Stowers, A.; Limpiboon, T.  
Mol. Biochem. Parasitol. 50, 139-149, 1992  
A:Title: The 42-kilodalton rhoptry-associated protein of Plasmodium falciparum.  
A:Reference number: A45633; MUID:92178281; PMID:1542308  
A:Accession: A45633  
A>Status: preliminary  
A:Molecule type: DNA; protein  
A:Residues: 1-398 <SAU>  
A:Cross-references: UNIPROT:Q26004  
A:Note: sequence extracted from NCBI backbone (NCBIN:85242, NCBI:85246)  
C:Superfamily: Plasmodium falciparum rhoptry-associated protein 2

Query Match 6.4%; Score 7; DB 2; Length 398;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 91 LRKRSS 97  
|||||  
Db 255 LRKRSS 261

RESULT 11  
F64084  
3-deoxy-manno-octulosonate cytidyltransferase (EC 2.7.7.38) [similarity] - Haemophilus  
C:Species: Haemophilus influenzae  
C:Date: 18-Aug-1995 #sequence\_revision 18-Aug-1995 #text\_change 09-Jul-2004  
C:Accession: F64084  
R:Feischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.  
.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.  
D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.  
Science 269, 496-512, 1995  
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,  
A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.  
A:Reference number: A64000; MUID:95350630; PMID:7542800  
A:Accession: F64084  
A>Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA

A;Residues: 1-427 <TIGR>  
A;Cross-references: UNIPROT:P44806; GB:U32748; GB:U42023; NID:g1573645; PIDN:AAC22311.1;  
C;Function:  
A;Description: catalyzes the transfer of 3-deoxy-D-manno-octulosonic acid from its CMP  
C;Superfamily: Chlamydia trachomatis 3-deoxy-manno-octulosonate cytidylyltransferase  
C;Keywords: nucleotidyltransferase; transmembrane protein

Query Match 6.4%; Score 7; DB 2; Length 427;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 VQGVLEV 26  
|||||  
Db 367 VQGVLEV 373

RESULT 12  
C64935  
hypothetical protein b1755 - Escherichia coli (strain K-12)  
C;Species: Escherichia coli  
C;Date: 12-Sep-1997 #sequence\_revision 17-Sep-1997 #text\_change 01-Mar-2002  
C;Accession: C64935  
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co  
.A.; Rose, D.J.; Mau, B.; Shao, Y.  
Science 277, 1453-1462, 1997  
A;Title: The complete genome sequence of Escherichia coli K-12.  
A;Reference number: A64720; MUID:97426617; PMID:9278503  
A;Accession: C64935  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-496 <BLAT>  
A;Cross-references: GB:AE000270; GB:U00096; NID:g1788045; PIDN:AAC74825.1; PID:g1788052;  
A;Experimental source: strain K-12, substrain MG1655

Query Match 6.4%; Score 7; DB 2; Length 496;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 SLLLMML 13  
|||||  
Db 227 SLLLMML 233

RESULT 13  
E90936  
probable transport system permease protein ECs2461 [imported] - Escherichia coli (strain  
C;Species: Escherichia coli  
C;Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 09-Jul-2004  
C;Accession: E90936  
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.  
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.  
DNA Res. 8, 11-22, 2001  
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene  
A;Reference number: A99629; MUID:21156231; PMID:11258796  
A;Accession: E90936  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-496 <HAY>  
A;Cross-references: UNIPROT:Q8DXS5; GB:BA000007; PIDN:BA835884.1; PID:g13361928; GSPDB:G  
A;Experimental source: strain O157:H7, substrain RMD 0509952  
C;Genetics:  
A;Gene: ECs2461

Query Match 6.4%; Score 7; DB 2; Length 496;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 SLLLMML 13  
|||||  
Db 227 SLLLMML 233

A85785  
probable transport system permease protein Z2787 [imported] - Escherichia coli (strain O1  
C;Species: Escherichia coli  
C;Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 09-Jul-2004  
C;Accession: A85785  
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew,  
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,  
Nature 409, 529-533, 2001  
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A;Reference number: A85480; MUID:21074935; PMID:11206551  
A;Accession: A85785  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-496 <STO>  
A;Cross-references: UNIPROT:Q8DXS5; GB:AE005174; NID:g12515777; PIDN:AAG56741.1; GSPDB:G  
A;Experimental source: strain O157:H7, substrain EDL933  
C;Genetics:  
A;Gene: Z2787

Query Match 6.4%; Score 7; DB 2; Length 496;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 SLLLMML 13  
|||||  
Db 227 SLLLMML 233

RESULT 15  
E95052  
hypothetical protein SP0453 [imported] - Streptococcus pneumoniae (strain TIGR4)  
C;Species: Streptococcus pneumoniae  
C;Date: 03-Aug-2001 #sequence\_revision 03-Aug-2001 #text\_change 09-Jul-2004  
C;Accession: E95052  
R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heide  
on, J.D.; Umavam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapfle, I  
nson, T.; Hickey, E.K.; Holt, I.E.  
Science 293, 498-506, 2001  
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,  
A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.  
A;Reference number: A95000; MUID:21357209; PMID:11463916  
A;Accession: E95052  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-521 <KOR>  
A;Cross-references: UNIPROT:Q97SD1; GB:AE005672; PIDN:AAK74614.1; PID:g14971923; GSPDB:G  
A;Experimental source: strain TIGR4  
C;Genetics:  
A;Gene: SP0453

Query Match 6.4%; Score 7; DB 2; Length 521;  
Best Local Similarity 100.0%; Pred. No. 35;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TSLLML 12  
|||||  
Db 10 TSLLML 16

Search completed: September 21, 2005, 13:45:12  
Job time : 42 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 21, 2005, 13:41:20 ; Search time 175 Seconds  
(without alignments)  
318.952 Million cell updates/sec

Title: US-10-700-314-2

Perfect score: 109

Sequence: 1 MKF1STSLMLLVSLSPV.....VLKRSSSTLPVPVFKRIP 109

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1612378 seqs, 512079187 residues

Word size : 6

Total number of hits satisfying chosen parameters: 2944

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : UniProt\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	109	100.0	109	1	SZ13_HUMAN
2	23	21.1	109	2	Q8HYN9 macaca mula
3	19	17.4	68	2	Q7YS87 macaca mula
4	9	8.3	849	2	Q7Z3L2 macaca mula
5	9	8.3	1139	1	RBL2_HUMAN
6	9	8.3	1139	2	Q8NE70
7	8	7.3	102	1	SECG_STRCO
8	8	7.3	102	2	Q9F9Q1
9	8	7.3	112	2	Q829W0
10	8	7.3	239	2	Q81BD9 arabidopsis
11	8	7.3	239	2	Q84WWS
12	8	7.3	354	2	Q74DB7 geobacter s
13	8	7.3	395	2	Q8FK19 escherichia
14	8	7.3	400	2	Q9W423 drosophila
15	8	7.3	405	2	Q73CG4 bacillus ce
16	8	7.3	583	2	Q7QQS3 giardia lam
17	8	7.3	787	2	Q6CVI2 kluyveromyc
18	7	6.4	74	2	Q95ZN4 caenorhabdi
19	7	6.4	76	2	Q8VN35 helicobacte
20	7	6.4	90	2	Q87BU4 xyella fas
21	7	6.4	90	2	Q9PB24 xyella fas
22	7	6.4	91	2	Q8QZ54 sabo virus.
23	7	6.4	94	2	Q20627 physarum po
24	7	6.4	120	2	Q6ZNP4 homo sapien
25	7	6.4	128	2	Q86CZ9 caenorhabdi
26	7	6.4	131	2	Q6XE6V semanga sup
27	7	6.4	154	2	Q8HJW5 aplysia pun
28	7	6.4	156	2	Q6Q0B8 aplysia cal
29	7	6.4	156	2	Q8P8J3 xanthomonas
30	7	6.4	169	2	Q837Q5 enterococu
31	7	6.4	180	2	Q8M172 tortanus fo

32 7 6.4 195 2 Q9NYD2 Q9nyd2 homo sapien  
33 7 6.4 206 2 Q8TMU2 Q8tmu2 methanosarc  
34 7 6.4 208 2 Q972X9 Q972x9 sulfolobus  
35 7 6.4 219 2 Q7YA30 Q7ya30 tortanus fo  
36 7 6.4 232 2 Q733J8 Q733j8 bacillus ce  
37 7 6.4 233 2 Q9T6J3 Q9t6j3 lepus comus  
38 7 6.4 235 2 Q98PJ3 Q98pj3 mycoplasma  
39 7 6.4 238 2 Q9T6I6 Q9t6i6 lepus olost  
40 7 6.4 242 2 Q6UXU8 Q6uxu8 homo sapien  
41 7 6.4 242 2 Q85JU4 Q85ju4 disogmus ar  
42 7 6.4 250 2 Q9PUY2 Q9puy2 apteronotus  
43 7 6.4 252 2 Q9VC67 Q9vc67 drosophila  
44 7 6.4 253 2 Q7VKQ1 Q7vkq1 haemophilus  
45 7 6.4 255 2 Q732H2 Q732h2 bacillus ce

#### ALIGNMENTS

RESULT 1  
SZ13\_HUMAN  
ID \_SZ13\_HUMAN STANDARD; PRT; 109 AA.  
AC O43927;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Small inducible cytokine B13 precursor (CXCL13) (B lymphocyte  
chemoattractant) (CXC chemokine BLC) (B cell-attracting chemokine 1)  
DE (BCA-1) (ANGIE).  
GN Name=CXCL13; Synonyms=BCAL, BLC, SCYB13;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98146056; PubMed=9486651; DOI=10.1038/35876;  
RA Gunn M.D., Ngo V.N., Ansel K.M., Ekland E.H., Cyster J.G.,  
RA Williams L.T.;  
RT "A B-cell-homing chemokine made in lymphoid follicles activates  
Burkitt's lymphoma receptor-1.";  
RL Nature 391:799-803(1998).  
[2]  
RN SEQUENCE FROM N.A.  
RP TISSUE=Periphereal blood leukocytes;  
RX MEDLINE=98130629; PubMed=9463416;  
RA Legler D.F., Loetscher M., Stuber Roos R., Clark-Lewis I.,  
RA Baggiolini M., Moser B.;  
RT "B cell-attracting chemokine 1, a human CXC chemokine expressed in  
lymphoid tissues, selectively attracts B lymphocytes via BLR1/CXCR5.";  
J. Exp. Med. 187:655-660(1998).  
[3]  
RN SEQUENCE FROM N.A.  
RP TISSUE=Periphereal blood;  
RA Napolitano M., Spinetti G., Gaetano C., Capogrossi C.M.;  
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.  
[4]  
RN SEQUENCE FROM N.A.  
RP TISSUE=Skeletal muscle;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.F., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.B.,  
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Hulyk S.W.,  
FAhey J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,  
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

```
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Chemotactic for B lymphocytes but not for T-
CC lymphocytes, monocytes and neutrophils. Does not induce calcium
CC release in B lymphocytes. Binds to BLR1/CXCR3.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Highest levels in liver, followed by spleen,
CC lymph node, appendix and stomach. Low levels in salivary gland,
CC mammary gland and fetal spleen.
CC -!- SIMILARITY: Belongs to the Interleukin alpha (chemokine Cx)
CC family.
CC -----
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CC -----
DR EMBL; AF044197; AAC14402.1; -
DR EMBL; AF044197; AAC14402.1; -
DR EMBL; AF029894; AAC17980.1; -
DR EMBL; BC012589; AAH12589.1; -
DR HSSP; P10145; 3IL8.
DR Genew; HGNC:10639; CXCL13.
DR H-InvDB; HIX0004315; -
DR MIM; 605149; -
DR GO; GO:0005625; C:soluble fraction; TAS.
DR GO; GO:0008009; F:chemokine activity; TAS.
DR GO; GO:0007267; P:cell-cell signaling; TAS.
DR GO; GO:0006935; P:chemotaxis; TAS.
DR GO; GO:0007204; P:cytosolic calcium ion concentration elevation; TAS.
DR GO; GO:0006955; P:immune response; TAS.
DR InterPro; IPR002473; C-X-C/Interlkn_8.
DR InterPro; IPR001811; Chemokine_IL8.
DR InterPro; IPR001089; CXCL13.
DR PRINTS; PR00436; INTERLEUKIN8.
DR PRINTS; PR00437; SMALLCYTCKXC.
DR PROSITE; PS00471; SMALL_CYTOKINES_CXC; FALSE NEG.
DR Chemotaxis; Cytokine; Inflammatory response; Signal.
DR SIGNAL 1 22 Potential.
FT CHAIN 23 109 Small inducible cytokine B13.
FT DISULFID 33 60 By similarity.
FT DISULFID 35 76 By similarity.
SQ SEQUENCE 109 AA; 12664 MW; 4057FCABEFF658A8 CRC64;

Query Match 100.0%; Score 109; DB 1; Length 109;
Best Local Similarity 100.0%; Pred. No. 3.2e-107;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKFISTLLMLVSSLPVQGVLEVYTSILRCVQESSVFIPRRFIDRIQLPRNGC 60
DB 1 MKFISTLLMLVSSLPVQGVLEVYTSILRCVQESSVFIPRRFIDRIQLPRNGC 60

QY 61 PRKEIIWKKNSIVCVDPQAEIQRWMEVLKRSSSTLPVPVKRKIP 109
DB 61 PRKEIIWKKNSIVCVDPQAEIQRWMEVLKRSSSTLPVPVKRKIP 109

RESULT 2
Q8HYN9 PRELIMINARY; PRT; 109 AA.
AC Q8HYN9;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
```

```
DE Chemokine CXCL13/BCA-1.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22123042; PubMed=12126650; DOI=10.1006/cyto.2002.0875;
RA Basu S., Schaefer T.M., Ghosh M., Fuller C.L., Reinhart T.A.;
RT "Molecular cloning and sequencing of 25 different rhesus macaque
RT chemokine cDNAs reveals evolutionary conservation among C, CC, CXCL
RT AND CX3C families of chemokines.";
RL Cytokine 18:140-148(2002).
DR EMBL; AF449284; AAN76087.1; -
DR HSSP; P02776; 1F9S.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008009; F:chemokine activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR002473; C-X-C/Interlkn_8.
DR InterPro; IPR001811; Chemokine_IL8.
DR InterPro; IPR001089; CXCL13.
DR Pfam; PF00048; IL8; 1.
DR PRINTS; PR00436; INTERLEUKIN8.
DR PRINTS; PR00437; SMALLCYTCKXC.
DR SMART; SM00199; SCY; 1.
DR SMART; SM00199; SCY; 1.
DR SEQUENCE 109 AA; 12614 MW; DDB6F9C947DCDECD CRC64;

Query Match 21.1%; Score 23; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. No. 4.8e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 SLLMLLVSSLPVQGVLEVYTT 29
DB 7 SLLMLLVSSLPVQGVLEVYTT 29

RESULT 3
Q7YS87 PRELIMINARY; PRT; 68 AA.
AC Q7YS87;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE BLC (Fragment).
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22308854; PubMed=12421572; DOI=10.1006/cyto.2002.1973;
RA Pachner A.R., Dail D., Narayan K., Dutta K., Cadavid D.;
RT "Increased expression of B-lymphocyte chemoattractant, but not pro-
RT inflammatory cytokines, in muscle tissue in rhesus chronic Lyme
RT borreliosis.";
RL Cytokine 19:297-307(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Pachner A.R., Narayan K.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY288934; AAP41949.1; -
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008009; F:chemokine activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
DR SMART; SM00199; SCY; 1.
FT NON_TER 1 1
SQ SEQUENCE 68 AA; 8030 MW; 4653D3BB4042EDF2 CRC64;

Query Match 17.4%; Score 19; DB 2; Length 68;
```

Best: Local Similarity 100.0%; Pred. No. 5.4e-12;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 55 PRNGCPRKEIIIVWKKNS 73  
Db 14 PRNGCPRKEIIIVWKKNS 32

## RESULT 4

Q723L2 PRELIMINARY; PRT; 849 AA.  
ID Q723L2  
AC Q723L2  
DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Hypothetical protein DKFZp781K2028.  
GN Name=DKFZp781K2028;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Human bone marrow;  
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,  
RA Fobo G., Han M., Wiemann S.;  
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BX537767; CAD97830.1; -;  
DR HSSP; P06400; IGUX.  
DR InterPro; IPR006670; Cyclin.  
DR InterPro; IPR011028; Cyclin\_like.  
DR InterPro; IPR002720; RB\_A.  
DR InterPro; IPR002719; RB\_B.  
DR Pfam; PF01858; RB\_A; 1.  
DR Pfam; PF01857; RB\_B; 1.  
DR SMART; SM00385; CYCLIN; 1.  
KW Hypothetical protein.  
SQ SEQUENCE 849 AA; 95258 NW; DA72742F2B3A9C117 CRC64;

Query Match 8.3%; Score 9; DB 2; Length 849;

Best: Local Similarity 100.0%; Pred. No. 2.3;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 94 RSSSTLPVP 102  
Db 680 RSSSTLPVP 688

## RESULT 5

RBL2 HUMAN  
ID RBL2 HUMAN STANDARD; PRT; 1139 AA.  
AC Q08999; Q15073; Q16084; Q92812;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE Retinoblastoma-like protein 2 (130 kDa retinoblastoma-associated protein) (PRB2) (P130) (RBR-2).  
DE protein (PRB2) (P130) (RBR-2).  
GN Name=RBL2; Synonyms=RB2;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Placenta, and Spleen;  
RX MEDLINE=94074895; PubMed=8253383;  
RA Li Y., Graham C., Lucy S., Duncan A.M.V., Whyte P.;  
RT "The adenovirus E1A-associated 130-kD protein is encoded by a member  
of the retinoblastoma gene family and physically interacts with  
cyclins A and E.";  
RT Cyclins A and E.";  
RL Genes Dev. 7:2366-2377(1993).  
RN [2]  
RP SEQUENCE FROM N.A.

RX MEDLINE=94074896; PubMed=8253384;  
RA Hannon G.J., Demetrick D., Beach D.;  
RT "Isolation of the RB-related p130 through its interaction with CDK2  
and cyclins.";  
RL Genes Dev. 7:2378-2391(1993).  
RN [3]  
RP SEQUENCE OF 58-1139 FROM N.A.  
RX MEDLINE=93368960; PubMed=8361765;  
RA Mayol X., Grana X., Baldi A., Sang N., Hu Q., Giordano A.;  
RT "Cloning of a new member of the retinoblastoma gene family (prb2)  
which binds to the E1A transforming domain.";  
RL Oncogene 8:2561-2566(1993).  
RN [4]  
RP SEQUENCE OF 1-80 FROM N.A.  
RX TISSUE=Placenta;  
RC TISSUE=Placenta;  
RX MEDLINE=96209782; PubMed=8643454; DOI=10.1073/pnas.93.10.4629;  
RA Baldi A., Boccia V., Claudio P.P., de Luca A., Giordano A.;  
RT "Genomic structure of the human retinoblastoma-related Rb2/p130  
gene.";  
RL Proc. Natl. Acad. Sci. U.S.A. 93:4629-4632(1996).  
RN [5]  
RP PHOSPHORYLATION SITE TVR-672.  
RX MEDLINE=22323103; PubMed=12435635; DOI=10.1101/gad.1011202;  
RA Tedesco D., Lukas J., Reed S.I.;  
RT "The prb2-related protein p130 is regulated by phosphorylation-  
dependent proteolysis via the protein-ubiquitin ligase SCF(Skp2).";  
RL Genes Dev. 16:2946-2957(2002).  
CC -!- FUNCTION: May have a function in cell cycle regulation. Binds to  
and may be involved in the transforming capacity of the adenovirus  
E1A protein. May act as a tumor suppressor. Potent inhibitor of  
E2F-mediated trans-activation, associates preferentially with  
E2F5. Binds to cyclins A and E.  
CC -!- SUBCELLULAR LOCATION: Nuclear.  
CC -!- PTM: Phosphorylation on Ser-672 in G1 leads to its ubiquitin-  
dependent proteolysis.  
CC -!- MISCELLANEOUS: G0-restricted expression.  
CC -!- SIMILARITY: Belongs to the retinoblastoma protein (RB) family.  
CC -----  
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CC -----  
DR EMBL; X76061; CAA53661.1; -;  
DR EMBL; S67171; AAB29227.1; -;  
DR EMBL; X74594; CAA52671.1; -;  
DR EMBL; U53220; AAC50479.1; -;  
DR PIR; A49370; A49370.  
DR HSSP; P06400; IGUX.  
DR TRANSFAC; T01608; -;  
DR Genew; HGNC:9894; RBL2.  
DR MIM; 180203; -;  
DR GO; GO:0005515; F:protein binding; TAS.  
DR InterPro; IPR006670; Cyclin.  
DR InterPro; IPR011028; Cyclin\_like.  
DR InterPro; IPR002720; RB\_A.  
DR InterPro; IPR002719; RB\_B.  
DR Pfam; PF01858; RB\_A; 1.  
DR Pfam; PF01857; RB\_B; 1.  
DR SMART; SM00385; CYCLIN; 2.  
KW Anti-oncogene; Cell cycle; DNA-binding; Nuclear protein;  
Phosphorylation; Transcription regulation.  
FT DOMAIN 417..1024 Pocket; binds E1A.  
FT DOMAIN 417..616 Domain A.  
FT DOMAIN 617..827 Spacer.  
FT DOMAIN 828..1024 Domain B.  
FT DOMAIN 9..16 Poly-Pro.  
FT DOMAIN 17..20 Poly-Ala.  
FT DOMAIN 23..26 Poly-Glu.  
FT DOMAIN 998..1001



```

FT MOD RES 672 672 Phosphoserine.
FT CONFLICT 37 37 S -> P (in Ref. 2).
FT CONFLICT 64 64 A -> P (in Ref. 1 and 4).
FT CONFLICT 206 206 V -> M (in Ref. 3).
SQ SEQUENCE 1139 AA; 128356 MW; ADPBD300DE9E1359 CRC64;

Query Match 8.3%; Score 9; DB 1; Length 1139;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 94 RSSSTLPVP 102
Db 970 RSSSTLPVP 978
|||||
|||||

RESULT 6
ID Q8NE70 PRELIMINARY; PRT; 1139 AA.
AC Q8NE70;
DT 01-OCT-2002 (T-EMBLrel. 22, Created)
DT 01-OCT-2002 (T-EMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE Retinoblastoma-like 2 (P130).
GN Name=RBL2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marasina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Phney J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Strausberg R.;
DR EMBL; BC034490; A034490.1; -.
DR HSSP; P06400; IGUX.
DR InterPro; IPR006670; Cyclin.
DR InterPro; IPR011028; Cyclin-like.
DR InterPro; IPR002720; RB_A.
DR InterPro; IPR002719; RB_B.
DR Pfam; PF01858; RB_A; 1.
DR Pfam; PF01857; RB_B; 1.
DR SMART; SM00385; CYCLIN; 2.
SQ SEQUENCE 1139 AA; 128346 MW; 4A55632FB1F39EE8 CRC64;

Query Match 8.3%; Score 9; DB 2; Length 1139;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 94 RSSSTLPVP 102
Db 970 RSSSTLPVP 978
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us-10-700-314-2.oli.rup

Db 970 RSSSTLPVP 978
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|||||

RESULT 7
ID -SECG_STRCO STANDARD; PRT; 102 AA.
AC Q9Z521;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Protein-export membrane protein secG.
GN Name=secG; OrderedLocusNames=SCO1944; ORFNames=SCC54.04c;
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RX MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Batsman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Larke L.D., Oliver K., O'Neil S.,
RA Rabinowitch E., Rajandream M.A., Rutherford K.M., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
coelicolor A3(2)."
RL Nature 417:141-147(2002).
CC -I- FUNCTION: Involved in protein export. Participates in an early
event of protein translocation (By similarity).
CC -I- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -I- SIMILARITY: Belongs to the secG family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AL939110; CAB38134.1; -.
CC PIR; T36017; T36017.
CC InterPro; IPR004692; SecG.
CC Pfam; PF03840; SecG; 1.
CC PRINTS; PR01651; SECSEXPORT.
CC TIGRFAMs; TIGR00810; secG; 1.
CC Complete proteome; Protein transport; Translocation; Transmembrane.
CC TRANSMEM 25 45 Potential.
CC TRANSMEM 79 99 Potential.
CC SEQUENCE 102 AA; 10716 MW; C3B4D9BD0EA70CDA CRC64;

Query Match 7.3%; Score 8; DB 1; Length 102;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 SLLMLLV 14
Db 37 SLLMLLV 44
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|||||

RESULT 8
ID Q9F9Q1 PRELIMINARY; PRT; 102 AA.
AC Q9F9Q1;
DT 01-MAR-2001 (T-EMBLrel. 16, Created)
DT 01-MAR-2001 (T-EMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)

```



DE SecG.  
 GN Name=secG;  
 OS Streptomyces lividans.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Streptomycineae; Streptomycetaceae; Streptomyces.  
 OX NCBI\_TaxID=1916;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Palacin A., Parro V., Mellado R.P.;  
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF182189; RAG16895.1; --  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0015450; F:protein translocase activity; IEA.  
 DR GO; GO:0009306; P:protein secretion; IEA.  
 DR InterPro; IPR004692; SecG.  
 DR Pfam; PF03840; SecG; 1.  
 DR PRINTS; PR01651; SECSEXPORT.  
 DR TIGRFAMs; TIGR00810; secG; 1.  
 SQ SEQUENCE 102 AA; 10760 MW; 86A498BA0ED00BAA CRC64;

Query Match 7.3%; Score 8; DB 2; Length 102;  
 Best Local Similarity 100.0%; Pred. No. 3.6;  
 \* Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 SLLMLLV 14  
 |||||  
 Db 37 SLLMLLV 44

## RESULT 9

Q829W0  
 ID Q829W0 PRELIMINARY; PRT; 112 AA.  
 AC Q829W0;  
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Putative SecG-like integral membrane protein.  
 GN Name=secG; OrderedLocusNames=SAV6299;  
 OS Streptomyces avermitilis.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Streptomycineae; Streptomycetaceae; Streptomyces.  
 OX NCBI\_TaxID=33903;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MA-4680;  
 RX MEDLINE=22608306; PubMed=12692562;  
 RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,  
 RA Sakaki Y., Hattori M., Omura S.;  
 RT "Complete genome sequence and comparative analysis of the industrial  
 RT microorganism Streptomyces avermitilis.";  
 RL Nat. Biotechnol. 21:526-531(2003).  
 RN [2]

SEQUENCE FROM N.A.  
 RC STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;  
 RX MEDLINE=21477403; PubMed=11572948; DOI=10.1073/pnas.2114333198;  
 RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,  
 RA Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osone T.,  
 RA Kikuchi H., Shiba T., Sakaki Y., Hattori M.;  
 RT "Genome sequence of an industrial microorganism Streptomyces  
 RT avermitilis: deducing the ability of producing secondary  
 RT metabolites.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).  
 DR EMBL; AP005046; BAC74010.1; --  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0015450; F:protein translocase activity; IEA.  
 DR GO; GO:0009306; P:protein secretion; IEA.  
 DR InterPro; IPR004692; SecG.  
 DR Pfam; PF03840; SecG; 1.  
 DR PRINTS; PR01651; SECSEXPORT.  
 DR TIGRFAMs; TIGR00810; secG; 1.  
 KW Complete proteome.  
 SQ SEQUENCE 112 AA; 11932 MW; C7B829FA18BEA6DF CRC64;

Query Match 7.3%; Score 8; DB 2; Length 112;  
 Best Local Similarity 100.0%; Pred. No. 4;  
 \* Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 7 SLLMLLV 14  
 |||||  
 Db 47 SLLMLLV 54

RESULT 10  
 Q8LBD9  
 ID Q8LBD9 PRELIMINARY; PRT; 239 AA.  
 AC Q8LBD9;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Putative proline-rich protein.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22088475; PubMed=12093376;  
 RA Haas B.J., Volfovsky N., Town C.D., Troukhan M., Alexandrov N.,  
 RA Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;  
 RT "Full-length messenger RNA sequences greatly improve genome  
 RT annotation.";  
 RL Genome Biol. 3:RESEARCH0029-RESEARCH0029(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,  
 RA Feldmann K.;  
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY087270; AAM64824.1; --  
 DR GO; GO:0005198; F:structural molecule activity; IEA.  
 DR InterPro; IPR000535; MSP.  
 DR InterPro; IPR008962; PapD-like.  
 DR InterPro; IPR008162; Pfam.  
 DR Pfam; PF00635; Motile\_Sperm; 1.  
 DR PROSITE; PS0202; MSP; 1.  
 DR PROSITE; PS00012; PHOSPHOPANTHETHEINE; UNKNOWN 1.  
 SQ SEQUENCE 239 AA; 26327 MW; 3D57A5E8B0EC76B CRC64;

Query Match 7.3%; Score 8; DB 2; Length 239;  
 Best Local Similarity 100.0%; Pred. No. 8.1;  
 \* Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 SLLMLLV 14  
 |||||  
 Db 218 SLLMLLV 225

## RESULT 11

Q84WW5  
 ID Q84WW5 PRELIMINARY; PRT; 239 AA.  
 AC Q84WW5;  
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Putative proline-rich protein.  
 GN Name=At4g00170;  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Yamada K., Chan M.M., Chang C.H., Dale J.M., Hsuan V.W., Lee J.M.,  
 RA Onodera C.S., Quach H.L., Tang C.C., Toriumi M., Wong C., Wu H.C.,  
 RA Yu G., Yuan S., Chen H., Cheuk R., Jones T., Kim C.J., Nguyen M.,

RA Palm C.J., Shinn P., Southwick A., Tripp M.G., Wu T., Davis R.W.,  
 RA Ecker J.R., Theologis A.;  
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BT001917; AAN71916.1; -.  
 DR GO: 0005198; F: structural molecule activity; IEA.  
 DR InterPro; IPR000535; MSP.  
 DR InterPro; IPR008962; PapD-like.  
 DR InterPro; IPR006162; Ppantne\_S.  
 DR Pfam; PF00635; Motile\_Sperm; 1.  
 DR PROSITE; PS0202; MSP; 1.  
 DR PROSITE; PS00012; PHOSPHOPANTHETINE; UNKNOWN 1.  
 SQ SEQUENCE 239 AA; 26374 MW; 2CA7AB2B7DF1E54B CRC64;

Query Match 7.3%; Score 8; DB 2; Length 239;  
 Best Local Similarity 100.0%; Pred. No. 8.1;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LLLMLLV 14  
 |||||

Db 218 LLLMLLV 225

## RESULT 12

Q74DB7 ID Q74DB7 PRELIMINARY; PRT; 354 AA.  
 AC Q74DB7  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Magnesium and cobalt transport protein CorA.  
 GN NamescorA-1; OrderedLocusNames=GSU1399;  
 OS Geobacter sulfurreducens.  
 OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales;  
 OC Geobacteraceae; Geobacter.  
 OX NCBI\_TaxID=35554;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=PCA / ATCC 51573;  
 RX PubMed=14671304; DOI=10.1126/science.1088727;  
 RA Methe B.A., Nelson K.E., Eisen J.A., Paulsen I.T., Nelson W.C.,  
 RA Heidelberg J.F., Wu D., Ward N.L., Beanan M.J., Dodson R.J.,  
 RA Madupu R., Brinkac L.M., Daugherty S.C., DeBoy R.T., Durkin A.S.,  
 RA Winn M.L., Kolonay J.F., Sullivan S.A., Haft D.H., Selengut J.,  
 RA Davidson T.M., Zafar N., White O., Tran B., Romero C., Forberger H.A.,  
 RA Weidman J.F., Khouri H.M., Feldblyum T.V., Utterback T.R.,  
 RA Van Aken S.E., Lovley D.R., Fraser C.M.;  
 RI "Genome of Geobacter sulfurreducens: metal reduction in subsurface  
 environments.";  
 RT Science 302.1967-1969(2003).  
 DR EMBL; AE017180; AAR34775.1; -.  
 DR TIGR; GSU1399; -.  
 DR GO: 0016020; C: membrane; IEA.  
 DR GO: 0015087; F: cobalt ion transporter activity; IEA.  
 DR GO: 0015095; F: magnesium ion transporter activity; IEA.  
 DR GO: 0006824; P: cobalt ion transport; IEA.  
 DR GO: 0015693; P: magnesium ion transport; IEA.  
 DR InterPro; IPR004488; CorA transp.  
 DR InterPro; IPR002523; Mg2+\_transpCorA.  
 DR Pfam; PF01544; CorA; 1.  
 DR TIGRFAMs; TIGR00383; corA; 1.  
 KW Complete proteome.  
 SQ SEQUENCE 354 AA; 41103 MW; A04ACC27EC8A6E3F CRC64;

Query Match 7.3%; Score 8; DB 2; Length 354;  
 Best Local Similarity 100.0%; Pred. No. 12;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LLLMLLV 15  
 |||||

Db 334 LLLMLLV 341

## RESULT 13

Q8FK19 ID Q8FK19 PRELIMINARY; PRT; 395 AA.  
 AC Q8FK19  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Isochorismate synthase entC (EC 5.4.99.6).  
 GN Name=entC; OrderedLocusNames=c0680;  
 OS Escherichia coli O6.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Escherichia.  
 OX NCBI\_TaxID=217992;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=06:HI / CFT073 / ATCC 700928;  
 RX MEDLINE=22388234; PubMed=12471157; DOI=10.1073/pnas.252529799;  
 RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,  
 RA Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,  
 RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,  
 RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.;  
 RT "Extensive mosaic structure revealed by the complete genome sequence  
 of uropathogenic Escherichia coli.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002).  
 DR EMBL; AE016757; AAN79155.1; -.  
 DR GO: 0008909; F: isochorismate synthase activity; IEA.  
 DR GO: 0016853; F: isomerase activity; IEA.  
 DR GO: 0009058; P: biosynthesis; IEA.  
 DR InterPro; IPR005801; Anth synth chor.  
 DR InterPro; IPR004561; Isochor synth.  
 DR Pfam; PF00425; Chorismate bind; 1.  
 DR PIRSF; PIRSF001502; Isochrmnt synth; 1.  
 DR ProDom; PD000779; Anth synth\_chor; 1.  
 DR TIGRFAMs; TIGR00543; Isochor\_syn; 1.  
 KW Complete proteome; Isomerase.  
 SQ SEQUENCE 395 AA; 43425 MW; 43BB8E87953DB245 CRC64;

Query Match 7.3%; Score 8; DB 2; Length 395;  
 Best Local Similarity 100.0%; Pred. No. 13;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 89 EVLRKSS 96  
 |||||

Db 255 EVLRKSS 262

RESULT 14  
 Q9W423 ID Q9W423 PRELIMINARY; PRT; 400 AA.  
 AC Q9W423; Q95RN6;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
 DE CG3576-PA (CG3576-pb) (LD18904p) (Longevity protein).  
 GN NamesLag1; Synonyms=CG15898, lon; ORFNames=CG3576;  
 OS Drosophila melanogaster (fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Vandal M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,  
 RA Wan X.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,  
 RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,  
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahle C., Davenport L.B., Davies P.,  
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,  
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merkulov G., Milshina N.V., Moadari C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,  
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,  
RA Williams S.M., Woodgett, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,  
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
RA "The genome sequence of Drosophila melanogaster.";  
RA Science 287:2185-2195 (2000).  
RA [2]  
RA SEQUENCE FROM N.A.  
RX MEDLINE=2426065; PubMed=12537558;  
RA Celnik S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,  
RA Patel S., Adams M., Champagne M., Dugan S.P., Frise E., Hodgson A.,  
RA George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,  
RA Pacle J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,  
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,  
RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;  
RA "Finishing a whole-genome shotgun: Release 3 of the Drosophila  
RA melanogaster euchromatic genome sequence.";  
RA Genome Biol. 3:RESEARCH0079-RESEARCH0079 (2002).  
RA [3]  
RA SEQUENCE FROM N.A.  
RX MEDLINE=2426070; PubMed=12537573;  
RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J., Svirskas R.,  
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,  
RA Ashburner M., Celnik S.E.;  
RA "The transposable elements of the Drosophila melanogaster euchromatin:  
RA a genomics perspective.";  
RA Genome Biol. 3:RESEARCH0084-RESEARCH0084 (2002).  
RA [4]  
RA SEQUENCE FROM N.A.  
RX MEDLINE=2426069; PubMed=12537572;  
RA Mira S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,  
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,  
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,  
RA Bettencourt B.R., Celnik S.E., de Grey A.D., Drysdale R.A.,  
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,  
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,  
RA Lewis S.E.;  
RA "Annotation of the Drosophila melanogaster euchromatic genome: a  
RA systematic review.";  
RA Genome Biol. 3:RESEARCH0083-RESEARCH0083 (2002).  
RA [5]  
RA SEQUENCE FROM N.A.  
RX FlyBase;  
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
RA [6]  
RA SEQUENCE FROM N.A.  
RX FlyBase;  
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.  
RA [7]  
RA SEQUENCE FROM N.A.  
RC STRAIN=Berkley;  
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,

RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,  
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,  
RA Nuncio J., Pacle J., Paragas V., Park S., Phouanavong S., Wan K.,  
RA Yu C., Lewis S.E., Rubin G.M., Celnik S.E.  
RA Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
RA [8]  
RA SEQUENCE FROM N.A.  
RX FlyBase;  
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).  
DR EMBL; AE003437; AAF46137.2; -;  
DR EMBL; AY061255; AAL28803.1; -;  
DR HSSP; P01367; 1LE8.  
DR IntAct; Q9W423; -;  
DR FlyBase; FBgn0040918; Lagl.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0005634; C:nucleus; IEA.  
DR GO; GO:0003700; P:transcription factor activity; IEA.  
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
DR InterPro; IPR001356; Homeobox.  
DR InterPro; IPR009057; Homeodomain\_like.  
DR InterPro; IPR005547; LAGL.  
DR InterPro; IPR006634; TUC.  
DR Pfam; PF03798; LAGL; 1.  
DR PRINTS; PR00024; HOMEBOX.  
DR SMART; SM00389; HOX; 1.  
DR SMART; SM00724; TUC; 1.  
DR PROSITE; PS50071; HOMEBOX\_2; 1.  
DR PROSITE; PS50922; TUC; 1.  
KW DNA-binding; Homeobox; Nuclear protein.  
SQ SEQUENCE 400 AA; 46350 MW; AB586DB2B8111E62 CRC64;  
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Best Local Similarity 100.0%; Pred. No. 13;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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ID Q73CG4 PRELIMINARY; PRT; 405 AA.  
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DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
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GN OrderedLocustNames=BCE1101;  
OS Bacillus cereus (strain ATCC 10987).  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=222523;  
RN [1]  
RX SEQUENCE FROM N.A.  
RA PubMed=14960714; DOI=10.1093/nar/gkh258;  
RA Rasko D.A., Ravel J., Oekstad O.A., Helgason E., Cer R.Z., Jiang L.,  
RA Shores K.A., Fouts D.E., Tourasse N.J., Angiuoli S.V., Kolonay J.F.,  
RA Nelson W.C., Kolstoe A.-B., Fraser C.M., Read T.D.;  
RA "The genome sequence of Bacillus cereus ATCC 10987 reveals metabolic  
RA adaptations and a large plasmid related to Bacillus anthracis pXO1.";  
RA Nucleic Acids Res. 32:977-988 (2004).  
DR EMBL; AE017267; AAS40032.1; -;  
DR TIGR; BCE1101; -;  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR InterPro; IPR003594; ATPbind\_ATPase.  
DR Pfam; PF02518; HATPase\_c; 1.  
DR SMART; SM00387; HATPase\_c; 1.  
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Query Match 7.3%; Score 8; DB 2; Length 405;

Best Local Similarity 100.0%; Pred. NO. 13;  
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Job time : 178 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 21, 2005, 13:41:21 ; Search time 63 Seconds  
(without alignments)  
704.196 Million cell updates/sec

Title: US-10-700-314-2

Perfect score: 109

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Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1826521 seqs, 407012169 residues

Word size : 6

Total number of hits satisfying chosen parameters: 2535

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications AA:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	109	100.0	109	14	US-10-247-287-4
2	109	100.0	109	14	US-10-050-902-240
3	109	100.0	109	14	US-10-050-898-240
4	109	100.0	109	14	US-10-247-671-158
5	109	100.0	109	15	US-10-058-270A-88
6	109	100.0	109	15	US-10-700-314-2
7	109	100.0	109	16	US-10-755-889-146
8	109	100.0	109	16	US-10-723-860-1494
9	109	100.0	109	17	US-10-510-121-10
10	109	100.0	109	18	US-10-756-149-5091
11	109	100.0	115	9	US-09-796-692-1143

12	109	100.0	115	9	US-09-796-692-1151	Sequence 1151, Ap
13	109	100.0	115	9	US-09-796-692-1167	Sequence 1167, Ap
14	109	100.0	115	9	US-09-796-692-1185	Sequence 1185, Ap
15	109	100.0	115	9	US-09-796-692-1200	Sequence 1200, Ap
16	109	100.0	115	9	US-09-796-692-1202	Sequence 1202, Ap
17	109	100.0	115	9	US-09-796-692-1245	Sequence 1245, Ap
18	109	100.0	115	9	US-09-796-692-1254	Sequence 1254, Ap
19	109	100.0	115	9	US-09-796-692-1315	Sequence 1315, Ap
20	109	100.0	115	9	US-09-796-692-1612	Sequence 1612, Ap
21	109	100.0	115	9	US-09-796-692-1662	Sequence 1662, Ap
22	109	100.0	115	9	US-09-796-692-1664	Sequence 1664, Ap
23	109	100.0	115	9	US-09-796-692-1707	Sequence 1707, Ap
24	109	100.0	115	9	US-09-796-692-1720	Sequence 1720, Ap
25	109	100.0	115	9	US-09-796-692-1795	Sequence 1795, Ap
26	109	100.0	115	9	US-09-796-692-2059	Sequence 2059, Ap
27	109	100.0	115	9	US-09-796-692-2215	Sequence 2215, Ap
28	109	100.0	115	9	US-09-796-692-2256	Sequence 2256, Ap
29	109	100.0	115	9	US-09-796-692-2266	Sequence 2266, Ap
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31	109	100.0	115	14	US-10-040-862-1151	Sequence 1151, Ap
32	109	100.0	115	14	US-10-040-862-1167	Sequence 1167, Ap
33	109	100.0	115	14	US-10-040-862-1185	Sequence 1185, Ap
34	109	100.0	115	14	US-10-040-862-1200	Sequence 1200, Ap
35	109	100.0	115	14	US-10-040-862-1202	Sequence 1202, Ap
36	109	100.0	115	14	US-10-040-862-1245	Sequence 1245, Ap
37	109	100.0	115	14	US-10-040-862-1254	Sequence 1254, Ap
38	109	100.0	115	14	US-10-040-862-1315	Sequence 1315, Ap
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41	109	100.0	115	14	US-10-040-862-1664	Sequence 1664, Ap
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44	109	100.0	115	14	US-10-040-862-1795	Sequence 1795, Ap
45	109	100.0	115	14	US-10-040-862-2059	Sequence 2059, Ap

#### ALIGNMENTS

#### RESULT 1

US-10-247-287-4  
; Sequence 4, Application US/10247287  
; Publication No. US20030082770A1

; GENERAL INFORMATION:

; APPLICANT: LI, HAODONG

; KREIDER, BRENT L.

; TITLE OF INVENTION: THERAPEUTIC COMPOSITIONS AND METHODS FOR

; TREATING DISEASE STATES WITH LEUKOCYTE ADHESION  
; INHIBITOR-1 (LAI-1), AND CHEMOKINE BETA-11 (CKBETA-11)

; NUMBER OF SEQUENCES: 16

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.

; STREET: 1100 NEW YORK AVENUE, SUITE 600

; CITY: WASHINGTON

; STATE: DC

; COUNTRY: USA

; ZIP: 20005

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/247,287

; FILING DATE: 20-Sep-2002

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/09/635,899

; FILING DATE: 11-Aug-2000

; APPLICATION NUMBER: US 08/943,336

; FILING DATE: 03-OCT-1997

; APPLICATION NUMBER: US 60/027,769

; FILING DATE: 04-OCT-1996

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; APPLICATION NUMBER: US 08/724,871
; FILING DATE: 04-OCT-1996
; APPLICATION NUMBER: PCT/US96/09572
; FILING DATE: 05-JUN-1996
; APPLICATION NUMBER: US 08/464,401
; FILING DATE: 05-JUN-1995
; APPLICATION NUMBER: US 08/460,987
; FILING DATE: 05-JUN-1995
; APPLICATION NUMBER: PCT/US95/01780
; FILING DATE: 08-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0380006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)371-2600
; TELEFAX: (202)371-2540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-247-287-4

Query Match      100.0%; Score 109; DB 14; Length 109;
Best Local Similarity 100.0%; Pred. No. 1.5e-96;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 PRKEIIVWKNKNSIVCVDPAEWIORMMEVLRKRSSSTLPVPVFKRKIP 109

RESULT 2
US-10-050-902-240
; Sequence 240, Application US/10050902
; Publication No. US20030175290A1
; GENERAL INFORMATION:
; APPLICANT: Renner, Wolfgang A.
; APPLICANT: Bachmann, Martin
; APPLICANT: Tissot, Alain
; APPLICANT: Maurer, Patrick
; APPLICANT: Lechner, Franziska
; APPLICANT: Sebbel, Peter
; APPLICANT: Plossek, Christine
; TITLE OF INVENTION: Molecular Antigen Array
; FILE REFERENCE: 1700.0190004
; CURRENT APPLICATION NUMBER: US/10/050,902
; CURRENT FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/262,379
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 60/288,549
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/326,998
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 60/331,045
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 240
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-050-902-240

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Best Local Similarity 100.0%; Pred. No. 1.5e-96;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 PRKEIIVWKNKNSIVCVDPAEWIORMMEVLRKRSSSTLPVPVFKRKIP 109

RESULT 3
US-10-050-898-240
; Sequence 240, Application US/10050898
; Publication No. US20030175711A1
; GENERAL INFORMATION:
; APPLICANT: Renner, Wolfgang A.
; APPLICANT: Bachmann, Martin
; APPLICANT: Tissot, Alain
; APPLICANT: Maurer, Patrick
; APPLICANT: Lechner, Franziska
; APPLICANT: Sebbel, Peter
; APPLICANT: Plossek, Christine
; APPLICANT: Ortmann, Rainer
; APPLICANT: Luond, Rainer
; APPLICANT: Staufenbiel, Matthias
; APPLICANT: Frey, Peter
; TITLE OF INVENTION: Molecular Antigen Array
; FILE REFERENCE: 1700.0190005
; CURRENT APPLICATION NUMBER: US/10/050,898
; CURRENT FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/262,379
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 60/288,549
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/326,998
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 60/331,045
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 240
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-050-898-240

Query Match      100.0%; Score 109; DB 14; Length 109;
Best Local Similarity 100.0%; Pred. No. 1.5e-96;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 PRKEIIVWKNKNSIVCVDPAEWIORMMEVLRKRSSSTLPVPVFKRKIP 109

RESULT 4
US-10-247-671-158
; Sequence 158, Application US/10247671
; Publication No. US20030194721A1
; GENERAL INFORMATION:
; APPLICANT: Mikita, Thomas
; APPLICANT: Shiffman, Dov
; APPLICANT: Porter, Gordon, J.
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED FOAM CELLS
; FILE REFERENCE: PA-0050 US
; CURRENT APPLICATION NUMBER: US/10/247,671
; CURRENT FILING DATE: 2002-09-18
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Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 PRKEIIVWKNKNSIVCVDPAEWIORMMEVLRKRSSSTLPVPVFKRKIP 109
Db 61 PRKEIIVWKNKNSIVCVDPAEWIORMMEVLRKRSSSTLPVPVFKRKIP 109

RESULT 3
US-10-050-898-240
; Sequence 240, Application US/10050898
; Publication No. US20030175711A1
; GENERAL INFORMATION:
; APPLICANT: Renner, Wolfgang A.
; APPLICANT: Bachmann, Martin
; APPLICANT: Tissot, Alain
; APPLICANT: Maurer, Patrick
; APPLICANT: Lechner, Franziska
; APPLICANT: Sebbel, Peter
; APPLICANT: Plossek, Christine
; APPLICANT: Ortmann, Rainer
; APPLICANT: Luond, Rainer
; APPLICANT: Staufenbiel, Matthias
; APPLICANT: Frey, Peter
; TITLE OF INVENTION: Molecular Antigen Array
; FILE REFERENCE: 1700.0190005
; CURRENT APPLICATION NUMBER: US/10/050,898
; CURRENT FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/262,379
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 60/288,549
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/326,998
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 60/331,045
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 350
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; SEQ ID NO 240
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-050-898-240

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Best Local Similarity 100.0%; Pred. No. 1.5e-96;
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RESULT 4
US-10-247-671-158
; Sequence 158, Application US/10247671
; Publication No. US20030194721A1
; GENERAL INFORMATION:
; APPLICANT: Mikita, Thomas
; APPLICANT: Shiffman, Dov
; APPLICANT: Porter, Gordon, J.
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED FOAM CELLS
; FILE REFERENCE: PA-0050 US
; CURRENT APPLICATION NUMBER: US/10/247,671
; CURRENT FILING DATE: 2002-09-18
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; PRIOR APPLICATION NUMBER: 60/323,784
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: PERL Program
; SEQ ID NO 158
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; FEATURE:
; OTHER INFORMATION: Incyte ID No. US20030194721A1 020293CD1
US-10-247-671-158

Query Match      100.0%; Score 109; DB 14; Length 109;
Best Local Similarity 100.0%; Pred. No. 1.5e-96;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MKFISTLLMLLVSSLSPPVQGVLEVYVTSLRRCVQESSVFIPRRFDRIQILPRGNGC 60

Qy 61 PRKEIIWKKNSIVCVDPOAEWIOQMMEVLKRSSSTLPVPVFKRKP 109
Db 61 PRKEIIWKKNSIVCVDPOAEWIOQMMEVLKRSSSTLPVPVFKRKP 109

RESULT 5
US-10-058-270A-88
; Sequence 88, Application US/10058270A
; Publication No. US20040029114A1
; GENERAL INFORMATION:
; APPLICANT: Mack, David H.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Afar, Daniel
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Breast Cancer, Compositions and
; FILE REFERENCE: 018501-005210US
; * CURRENT APPLICATION NUMBER: US/10/058,270A
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: US 60/263,965
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: US 60/265,928
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 09/829,472
; PRIOR FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: US 60/282,698
; PRIOR FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: US 60/288,590
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/294,443
; PRIOR FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 88
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-058-270A-88

Query Match      100.0%; Score 109; DB 15; Length 109;
Best Local Similarity 100.0%; Pred. No. 1.5e-96;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKFISTLLMLLVSSLSPPVQGVLEVYVTSLRRCVQESSVFIPRRFDRIQILPRGNGC 60
Db 1 MKFISTLLMLLVSSLSPPVQGVLEVYVTSLRRCVQESSVFIPRRFDRIQILPRGNGC 60

Qy 61 PRKEIIWKKNSIVCVDPOAEWIOQMMEVLKRSSSTLPVPVFKRKP 109
Db 61 PRKEIIWKKNSIVCVDPOAEWIOQMMEVLKRSSSTLPVPVFKRKP 109

RESULT 6
US-10-700-314-2
; Sequence 2, Application US/10700314
; Publication No. US20040086975A1
; GENERAL INFORMATION:
; APPLICANT: GUEGLER, Karl J.
; APPLICANT: HAWKINS, Phillip R.
; APPLICANT: WILDE, Craig G.
; APPLICANT: SEILHAMER, Jeffrey J.
; TITLE OF INVENTION: CHEMOKINE EXPRESSED IN INFLAMED ADENOID
; FILE REFERENCE: PP-0025-4 DIV
; CURRENT APPLICATION NUMBER: US/10/700,314
; CURRENT FILING DATE: 2003-10-28
; PRIOR APPLICATION NUMBER: US 09/588,044
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: US 09/203,235
; PRIOR FILING DATE: 1998-12-01
; PRIOR APPLICATION NUMBER: US 08/862,607
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: US 08/352,324
; PRIOR FILING DATE: 1994-12-07
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PERL Program
; SEQ ID NO 2
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 020293CD1
US-10-700-314-2

Query Match      100.0%; Score 109; DB 15; Length 109;
Best Local Similarity 100.0%; Pred. No. 1.5e-96;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKFISTLLMLLVSSLSPPVQGVLEVYVTSLRRCVQESSVFIPRRFDRIQILPRGNGC 60
Db 1 MKFISTLLMLLVSSLSPPVQGVLEVYVTSLRRCVQESSVFIPRRFDRIQILPRGNGC 60

Qy 61 PRKEIIWKKNSIVCVDPOAEWIOQMMEVLKRSSSTLPVPVFKRKP 109
Db 61 PRKEIIWKKNSIVCVDPOAEWIOQMMEVLKRSSSTLPVPVFKRKP 109

RESULT 7
US-10-755-889-146
; Sequence 146, Application US/10755889
; Publication No. US20040171823A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-kB
; TITLE OF INVENTION: PATHWAY
; FILE REFERENCE: D0284 NP
; CURRENT APPLICATION NUMBER: US/10/755,889
; CURRENT FILING DATE: 2004-01-13
; PRIOR APPLICATION NUMBER: U.S. 60/440,068
; PRIOR FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: U.S. 60/469,757
; PRIOR FILING DATE: 2003-05-12
; NUMBER OF SEQ ID NOS: 823
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 146
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-755-889-146

Query Match      100.0%; Score 109; DB 16; Length 109;
Best Local Similarity 100.0%; Pred. No. 1.5e-96;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKFISTLLMLLVSSLSPPVQGVLEVYVTSLRRCVQESSVFIPRRFDRIQILPRGNGC 60
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Db 1 MKFISTLLMLLVSSLPVQGVLEVYVTSLRRCVQESSVFIPRRFIDRIQLPRGNC 60  
QY 61 PRKEIIVWKKNSIVCVDPOAEWIORMMEVLRKRSSSTLPVPVFKRKIP 109  
Db 61 PRKEIIVWKKNSIVCVDPOAEWIORMMEVLRKRSSSTLPVPVFKRKIP 109

RESULT 8  
US-10-723-860-1494  
; Sequence 1494, Application US/10723860  
; Publication No. US20040253606A1  
; GENERAL INFORMATION:  
; APPLICANT: Aziz, Natasha  
; APPLICANT: Ginsburg, Wendy M.  
; APPLICANT: Zlotnik, Albert  
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &  
; FILE REFERENCE: 05882.0193.NPUS01  
; CURRENT APPLICATION NUMBER: US/10/723,860  
; CURRENT FILING DATE: 2003-11-26  
; PRIOR APPLICATION NUMBER: 60/429,739  
; PRIOR FILING DATE: 2002-11-26  
; NUMBER OF SEQ ID NOS: 8393  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1494  
; LENGTH: 109  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-723-860-1494

Query Match 100.0%; Score 109; DB 16; Length 109;  
Best Local Similarity 100.0%; Pred. No. 1.5e-96;  
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MKFISTLLMLLVSSLPVQGVLEVYVTSLRRCVQESSVFIPRRFIDRIQLPRGNC 60  
Db 1 MKFISTLLMLLVSSLPVQGVLEVYVTSLRRCVQESSVFIPRRFIDRIQLPRGNC 60  
QY 61 PRKEIIVWKKNSIVCVDPOAEWIORMMEVLRKRSSSTLPVPVFKRKIP 109  
Db 61 PRKEIIVWKKNSIVCVDPOAEWIORMMEVLRKRSSSTLPVPVFKRKIP 109

RESULT 9  
US-10-510-121-10  
; Sequence 10, Application US/10510121  
; Publication No. US20050119174A1  
; GENERAL INFORMATION:  
; APPLICANT: SUGARU, Eiji  
; APPLICANT: ICHIHARA, Junji  
; APPLICANT: taiji, Matsuo  
; TITLE OF INVENTION: Novel Blood Sugar Controller and Method of Screening the Same  
; FILE REFERENCE: 231060  
; CURRENT APPLICATION NUMBER: US/10/510,121  
; CURRENT FILING DATE: 2004-10-04  
; PRIOR APPLICATION NUMBER: JP 2002-101781  
; PRIOR FILING DATE: 2002-04-03  
; PRIOR APPLICATION NUMBER: PCT/JP03/04260  
; PRIOR FILING DATE: 2003-04-03  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 10  
; LENGTH: 109  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-510-121-10

Query Match 100.0%; Score 109; DB 17; Length 109;  
Best Local Similarity 100.0%; Pred. No. 1.5e-96;  
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MKFISTLLMLLVSSLPVQGVLEVYVTSLRRCVQESSVFIPRRFIDRIQLPRGNC 60

Db 1 MKFISTLLMLLVSSLPVQGVLEVYVTSLRRCVQESSVFIPRRFIDRIQLPRGNC 60  
QY 61 PRKEIIVWKKNSIVCVDPOAEWIORMMEVLRKRSSSTLPVPVFKRKIP 109  
Db 61 PRKEIIVWKKNSIVCVDPOAEWIORMMEVLRKRSSSTLPVPVFKRKIP 109

RESULT 10  
US-10-756-149-5091  
; Sequence 5091, Application US/10756149  
; Publication No. US20050181375A1  
; GENERAL INFORMATION:  
; APPLICANT: Aziz, Natasha  
; APPLICANT: Zlotnik, Albert  
; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS AND  
; FILE REFERENCE: file  
; CURRENT APPLICATION NUMBER: US/10/756,149  
; CURRENT FILING DATE: 2004-01-12  
; NUMBER OF SEQ ID NOS: 5818  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 5091  
; LENGTH: 109  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-756-149-5091

Query Match 100.0%; Score 109; DB 18; Length 109;  
Best Local Similarity 100.0%; Pred. No. 1.5e-96;  
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MKFISTLLMLLVSSLPVQGVLEVYVTSLRRCVQESSVFIPRRFIDRIQLPRGNC 60  
Db 1 MKFISTLLMLLVSSLPVQGVLEVYVTSLRRCVQESSVFIPRRFIDRIQLPRGNC 60  
QY 61 PRKEIIVWKKNSIVCVDPOAEWIORMMEVLRKRSSSTLPVPVFKRKIP 109  
Db 61 PRKEIIVWKKNSIVCVDPOAEWIORMMEVLRKRSSSTLPVPVFKRKIP 109

RESULT 11  
US-09-796-692-1143  
; Sequence 1143, Application US/09796692  
; Publication No. US20020198362A1  
; GENERAL INFORMATION:  
; APPLICANT: Gaiger, Alexander  
; APPLICANT: Algate, Paul A.  
; APPLICANT: Mannion, Jane  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY  
; FILE REFERENCE: 2077.001200  
; CURRENT APPLICATION NUMBER: US/09/796,692  
; CURRENT FILING DATE: 2001-03-01  
; PRIOR APPLICATION NUMBER: 60/186,126  
; PRIOR FILING DATE: 2000-03-01  
; PRIOR APPLICATION NUMBER: 60/190,479  
; PRIOR FILING DATE: 2000-03-17  
; PRIOR APPLICATION NUMBER: 60/200,545  
; PRIOR FILING DATE: 2000-04-27  
; PRIOR APPLICATION NUMBER: 60/200,303  
; PRIOR FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: 60/200,779  
; PRIOR FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: 60/200,999  
; PRIOR FILING DATE: 2000-05-01  
; PRIOR APPLICATION NUMBER: 60/202,084  
; PRIOR FILING DATE: 2000-05-04  
; PRIOR APPLICATION NUMBER: 60/206,201  
; PRIOR FILING DATE: 2000-05-22  
; PRIOR APPLICATION NUMBER: 60/218,950  
; PRIOR FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: 60/222,903

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; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,378
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 9597
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1143
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-796-692-1143

Query Match      100.0%; Score 109; DB 9; Length 115;
Best Local Similarity 100.0%; Pred. No. 1.6e-96;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKFISTSLMLLVSSLSPPVQGVLEVYVTSLRRCVQVSSVFIPIRRFIDRIQILPRGNCG 60
DB 7 MKFISTSLMLLVSSLSPPVQGVLEVYVTSLRRCVQVSSVFIPIRRFIDRIQILPRGNCG 66

QY 61 PRKEIIVWKNKSIVCDPQAEWIQRMMEVLKRKSSSTLPVPVFKRKIP 109
DB 67 PRKEIIVWKNKSIVCDPQAEWIQRMMEVLKRKSSSTLPVPVFKRKIP 115

RESULT 12
US-09-796-692-1151
; Sequence 1151, Application US/09796692
; Publication No. US20020198362A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Mannion, Paul A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
; FILE REFERENCE: 2077.001200
; CURRENT APPLICATION NUMBER: US/09/796,692
; PRIOR FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,999
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,378
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 9597
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1151
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-796-692-1151

Query Match      100.0%; Score 109; DB 9; Length 115;
Best Local Similarity 100.0%; Pred. No. 1.6e-96;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKFISTSLMLLVSSLSPPVQGVLEVYVTSLRRCVQVSSVFIPIRRFIDRIQILPRGNCG 60
DB 7 MKFISTSLMLLVSSLSPPVQGVLEVYVTSLRRCVQVSSVFIPIRRFIDRIQILPRGNCG 66

QY 61 PRKEIIVWKNKSIVCDPQAEWIQRMMEVLKRKSSSTLPVPVFKRKIP 109
DB 67 PRKEIIVWKNKSIVCDPQAEWIQRMMEVLKRKSSSTLPVPVFKRKIP 115

RESULT 13
US-09-796-692-1167
; Sequence 1167, Application US/09796692
; Publication No. US20020198362A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Mannion, Paul A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
; FILE REFERENCE: 2077.001200
; CURRENT APPLICATION NUMBER: US/09/796,692
; PRIOR FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,378
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 9597
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1167
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-796-692-1167

Query Match      100.0%; Score 109; DB 9; Length 115;
Best Local Similarity 100.0%; Pred. No. 1.6e-96;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKFISTSLMLLVSSLSPPVQGVLEVYVTSLRRCVQVSSVFIPIRRFIDRIQILPRGNCG 60
DB 7 MKFISTSLMLLVSSLSPPVQGVLEVYVTSLRRCVQVSSVFIPIRRFIDRIQILPRGNCG 66

QY 61 PRKEIIVWKNKSIVCDPQAEWIQRMMEVLKRKSSSTLPVPVFKRKIP 109
DB 67 PRKEIIVWKNKSIVCDPQAEWIQRMMEVLKRKSSSTLPVPVFKRKIP 115

RESULT 14
US-09-796-692-1185
; Sequence 1185, Application US/09796692
; Publication No. US20020198362A1
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Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKFISTSLMLLVSSLSPPVQGVLEVYVTSLRRCVQVSSVFIPIRRFIDRIQILPRGNCG 60
DB 7 MKFISTSLMLLVSSLSPPVQGVLEVYVTSLRRCVQVSSVFIPIRRFIDRIQILPRGNCG 66

QY 61 PRKEIIVWKNKSIVCDPQAEWIQRMMEVLKRKSSSTLPVPVFKRKIP 109
DB 67 PRKEIIVWKNKSIVCDPQAEWIQRMMEVLKRKSSSTLPVPVFKRKIP 115
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RESULT 13
US-09-796-692-1167
; Sequence 1167, Application US/09796692
; Publication No. US20020198362A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Mannion, Paul A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
; FILE REFERENCE: 2077.001200
; CURRENT APPLICATION NUMBER: US/09/796,692
; PRIOR FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,378
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 9597
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1167
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-796-692-1167
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Query Match      100.0%; Score 109; DB 9; Length 115;
Best Local Similarity 100.0%; Pred. No. 1.6e-96;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKFISTSLMLLVSSLSPPVQGVLEVYVTSLRRCVQVSSVFIPIRRFIDRIQILPRGNCG 60
DB 7 MKFISTSLMLLVSSLSPPVQGVLEVYVTSLRRCVQVSSVFIPIRRFIDRIQILPRGNCG 66

QY 61 PRKEIIVWKNKSIVCDPQAEWIQRMMEVLKRKSSSTLPVPVFKRKIP 109
DB 67 PRKEIIVWKNKSIVCDPQAEWIQRMMEVLKRKSSSTLPVPVFKRKIP 115
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RESULT 14
US-09-796-692-1185
; Sequence 1185, Application US/09796692
; Publication No. US20020198362A1
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; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
; FILE REFERENCE: 2077.001200
; CURRENT APPLICATION NUMBER: US/09/796,692
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/202,084
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/222,903
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/222,416
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 60/223,378
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 60/223,378
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 9597
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1185
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-796-692-1185

Query Match      100.0%; Score 109; DB 9; Length 115;
Best Local Similarity 100.0%; Pred. No. 1.6e-96;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MKFISTLLMLLVSSLPVQGVLEVYVYTSLRRCVQESSVFIPRRFIDRIQLPRGNGC 60
      |||
Db      7 MKFISTLLMLLVSSLPVQGVLEVYVYTSLRRCVQESSVFIPRRFIDRIQLPRGNGC 66

QY      61 PRKEIIVWKKNSIVCVDPOAEWIQRMMEVLRKRSSSTLPVPVFKRKIP 109
      |||
Db      67 PRKEIIVWKKNSIVCVDPOAEWIQRMMEVLRKRSSSTLPVPVFKRKIP 115

RESULT 15
US-09-796-692-1200
; Sequence 1200, Application US/09796692
; Publication No. US20020198362A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
; FILE REFERENCE: 2077.001200
; CURRENT APPLICATION NUMBER: US/09/796,692
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/200,545
; PRIOR FILING DATE: 2000-04-27
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; PRIOR APPLICATION NUMBER: 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,378
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 9597
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1200
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-796-692-1200

Query Match      100.0%; Score 109; DB 9; Length 115;
Best Local Similarity 100.0%; Pred. No. 1.6e-96;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MKFISTLLMLLVSSLPVQGVLEVYVYTSLRRCVQESSVFIPRRFIDRIQLPRGNGC 60
      |||
Db      7 MKFISTLLMLLVSSLPVQGVLEVYVYTSLRRCVQESSVFIPRRFIDRIQLPRGNGC 66

QY      61 PRKEIIVWKKNSIVCVDPOAEWIQRMMEVLRKRSSSTLPVPVFKRKIP 109
      |||
Db      67 PRKEIIVWKKNSIVCVDPOAEWIQRMMEVLRKRSSSTLPVPVFKRKIP 115
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Search completed: September 21, 2005, 13:46:20  
Job time : 64 secs

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OM protein - protein search, using sw model

Run on: September 21, 2005, 13:41:21 ; Search time 43 Seconds  
(without alignments)  
189.227 Million cell updates/sec

Title: US-10-700-314-2  
Perfect score: 109  
Sequence: 1 MKFISTSLMLLVSLSPV.....VLKRSSSTLPVPVFKRIP 109

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 513545 seqs, 74649064 residues

Word size : 6

Total number of hits satisfying chosen parameters: 427

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents\_AA\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	109	100.0	109	1	US-08-352-324A-2
2	109	100.0	109	1	US-08-352-324A-9
3	109	100.0	109	2	US-08-862-607-2
4	109	100.0	109	2	US-08-862-607-9
5	109	100.0	109	3	US-09-203-235-2
6	109	100.0	109	3	US-09-203-235-9
7	109	100.0	109	3	US-08-982-493-4
8	109	100.0	109	3	US-08-943-336A-4
9	109	100.0	109	4	US-09-635-899-4
10	109	100.0	109	4	US-09-588-044-2
11	109	100.0	109	4	US-09-588-044-9
12	109	100.0	109	5	PCT-US95-01780-4
13	109	100.0	109	5	PCT-US95-16144-2
14	109	100.0	109	5	PCT-US95-16144-9
15	109	100.0	115	4	US-09-949-016-7722
16	72	66.1	72	4	US-09-567-225-19
17	9	8.3	195	3	US-09-213-293D-19
18	9	8.3	1082	1	US-08-106-493A-2
19	9	8.3	1082	1	US-08-429-284-2
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21	9	8.3	1139	2	US-08-832-877-2
22	7	6.4	162	4	US-09-311-021-134
23	7	6.4	180	4	US-09-134-000C-5693
24	7	6.4	442	3	US-08-821-994-66
25	7	6.4	443	3	US-08-821-994-65
26	7	6.4	521	4	US-09-583-110-4712
27	7	6.4	521	4	US-10-140-372-8

28	7	6.4	570	2	US-08-484-993B-16	Sequence 16, Appl
29	7	6.4	570	2	US-08-484-158B-16	Sequence 16, Appl
30	7	6.4	570	2	US-08-484-596A-16	Sequence 16, Appl
31	7	6.4	570	2	US-08-480-150A-16	Sequence 16, Appl
32	7	6.4	570	3	US-08-458-731-16	Sequence 16, Appl
33	7	6.4	570	3	US-08-149-223A-16	Sequence 16, Appl
34	6	5.5	11	4	US-09-817-310-5	Sequence 5, Appli
35	6	5.5	11	4	US-10-355-724A-5	Sequence 5, Appli
36	6	5.5	26	4	US-09-149-476-349	Sequence 349, App
37	6	5.5	30	4	US-09-402-532-9	Sequence 9, Appli
38	6	5.5	33	4	US-09-402-532-10	Sequence 10, Appl
39	6	5.5	42	4	US-09-471-276-1267	Sequence 1267, Ap
40	6	5.5	59	4	US-09-270-767-42049	Sequence 42049, A
41	6	5.5	60	4	US-09-288-143-68	Sequence 68, Appl
42	6	5.5	67	4	US-09-489-039A-8603	Sequence 8603, Ap
43	6	5.5	73	4	US-09-248-796A-22923	Sequence 22923, A
44	6	5.5	76	4	US-09-621-976-5766	Sequence 5766, Ap
45	6	5.5	82	4	US-09-599-632-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1  
US-08-352-324A-2  
; Sequence 2, Application US/08352324A  
; Patent No. 5633149  
; GENERAL INFORMATION:  
; APPLICANT: Guegler, Karl J.  
; APPLICANT: Hawkins, Phillip R.  
; APPLICANT: Wilde, Craig G.  
; APPLICANT: Seilhamer, Jeffrey J.  
; TITLE OF INVENTION: A NOVEL CHEMOKINE EXPRESSED IN  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: US  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/352,324A  
; FILING DATE: 07-DEC-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Luther, Barbara J.  
; REGISTRATION NUMBER: 33,954  
; REFERENCE/DOCKET NUMBER: PF-0025 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-855-0555  
; TELEFAX: 415-852-0195  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 109 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: polypeptide  
; IMMEDIATE SOURCE:  
; LIBRARY: Inflamed Adenoid  
; CLONE: 20293  
US-08-352-324A-2

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Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



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; STATE: CA
; COUNTRY: US
; ZIP: 94304
; COMPUTER READABLE FORM:
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; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/862,607
; FILING DATE: 23-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/352,324
; FILING DATE: 07-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Luther, Barbara J.
; REGISTRATION NUMBER: 33,954
; REFERENCE/DOCKET NUMBER: PF-0025 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-852-0195
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-862-607-9

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Best Local Similarity 100.0%; Pred. No. 6e-98;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 5
US-09-203-235-2
; Sequence 2, Application US/09203235
; Patent No. 6071701
; GENERAL INFORMATION:
; APPLICANT: Guegler, Karl J.
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Wilde, Craig G.
; APPLICANT: Seilhamer, Jeffrey J.
; TITLE OF INVENTION: A NOVEL CHEMOKINE EXPRESSED IN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/203,235
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
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; APPLICATION NUMBER: 08/862,607
; FILING DATE: 23-MAY-1997
; APPLICATION NUMBER: 08/352,324
; FILING DATE: 07-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Luther, Barbara J.
; REGISTRATION NUMBER: 33,954
; REFERENCE/DOCKET NUMBER: PF-0025 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-852-0195
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: polypeptide
; IMMEDIATE SOURCE:
; LIBRARY: Inflamed Adenoid
; CLONE: 20293
; US-09-203-235-2

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Best Local Similarity 100.0%; Pred. No. 6e-98;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 PRKEIIWKNKSI VCDPQAEWIQRMMEVLKRKSSSTLPVPVFKRKIP 109

RESULT 6
US-09-203-235-9
; Sequence 9, Application US/09203235
; Patent No. 6071701
; GENERAL INFORMATION:
; APPLICANT: Guegler, Karl J.
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Wilde, Craig G.
; APPLICANT: Seilhamer, Jeffrey J.
; TITLE OF INVENTION: A NOVEL CHEMOKINE EXPRESSED IN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/203,235
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/862,607
; FILING DATE: 23-MAY-1997
; APPLICATION NUMBER: 08/352,324
; FILING DATE: 07-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Luther, Barbara J.
; REGISTRATION NUMBER: 33,954
; REFERENCE/DOCKET NUMBER: PF-0025 US
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; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-855-0555  
; TELEFAX: 415-852-0195  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 109 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-09-203-235-9

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Best Local Similarity 100.0%; Pred. No. 6e-98; Indels 0; Gaps 0;  
Matches 109; Conservative 0; Mismatches 0;  
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RESULT 7  
US-08-982-493-4

; Sequence 4, Application US/08982493  
; Patent No. 6110695  
; GENERAL INFORMATION:  
; APPLICANT: Gunn, Michael D  
; APPLICANT: Williams, Lewis T  
; APPLICANT: Cyster, Jason G  
; TITLE OF INVENTION: Modulating B Lymphocyte Chemokine /  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
; STREET: 75 DENISE DRIVE  
; CITY: HILLSBOROUGH  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94010  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/982,493  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: OSMAN, RICHARD A  
; REGISTRATION NUMBER: 36,627  
; REFERENCE/DOCKET NUMBER: UCSF98-026  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 343-4341  
; TELEFAX: (650) 343-4342  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 109 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-982-493-4

Query Match 100.0%; Score 109; DB 3; Length 109;  
Best Local Similarity 100.0%; Pred. No. 6e-98; Indels 0; Gaps 0;  
Matches 109; Conservative 0; Mismatches 0;  
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Db 1 MKFISTLLMLVSSLSPPQGVLEVYVTSRLRCRCQVSSVFIPRRFIDRIQLPRGNC 60  
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DB 61 PRKEIIVWKNKSIIVCVDPOAEWIOQMMEVLRKRSSSTLPPVPFKRKIP 109  
RESULT 8  
US-08-943-336A-4  
; Sequence 4, Application US/08943336A  
; Patent No. 6139832  
; GENERAL INFORMATION:  
; APPLICANT: LI, HAODONG  
; APPLICANT: KREIDER, BRENT L.  
; TITLE OF INVENTION: THERAPEUTIC COMPOSITIONS AND METHODS FOR  
; TITLE OF INVENTION: TREATING DISEASE STATES WITH LEUKOCYTE ADHESION  
; TITLE OF INVENTION: INHIBITOR-1 (LAI-1), AND CHEMOKINE BETA-11 (CKBETA-11)  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.  
; STREET: 1100 NEW YORK AVENUE, SUITE 600  
; CITY: WASHINGTON  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/943,336A  
; FILING DATE: 03-OCT-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/027,769  
; FILING DATE: 04-OCT-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/724,871  
; FILING DATE: 04-OCT-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US96/09572  
; FILING DATE: 05-JUN-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/464,401  
; FILING DATE: 05-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/460,987  
; FILING DATE: 05-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/01780  
; FILING DATE: 08-FEB-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: STEFFE, ERIC K.  
; REGISTRATION NUMBER: 36,688  
; REFERENCE/DOCKET NUMBER: 1488.0380005  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)371-2600  
; TELEFAX: (202)371-2540  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 109 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-943-336A-4

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Best Local Similarity 100.0%; Pred. No. 6e-98; Indels 0; Gaps 0;  
Matches 109; Conservative 0; Mismatches 0;  
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DB 1 MKFISTLLMLVSSLSPPQGVLEVYVTSRLRCRCQVSSVFIPRRFIDRIQLPRGNC 60



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Db 61 PRKEIIVWKNKNSIVCVDPOAEWIOQMMEVLKRKSSSTLPVPVFKRKIP 109

RESULT 9  
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; Sequence 4, Application US/09635899  
; Patent No. 6485719  
; GENERAL INFORMATION:  
; APPLICANT: LI, HAODONG  
; KREIDER, BRENT L.  
; TITLE OF INVENTION: THERAPEUTIC COMPOSITIONS AND METHODS FOR  
; TREATING DISEASE STATES WITH LEUKOCYTE ADHESION  
; INHIBITOR-1 (LAI-1), AND CHEMOKINE BETA-11 (CRBETA-11)  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.  
; STREET: 1100 NEW YORK AVENUE, SUITE 600  
; CITY: WASHINGTON  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
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; APPLICATION NUMBER: US/09/635,899.  
; FILING DATE: 11-Aug-2000  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/943,336  
; FILING DATE: 03-OCT-1997  
; APPLICATION NUMBER: US 60/027,769  
; FILING DATE: 04-OCT-1996  
; APPLICATION NUMBER: US 08/724,871  
; FILING DATE: 04-OCT-1996  
; APPLICATION NUMBER: PCT/US96/09572  
; FILING DATE: 05-JUN-1996  
; APPLICATION NUMBER: US 08/464,401  
; FILING DATE: 05-JUN-1995  
; APPLICATION NUMBER: US 08/460,987  
; FILING DATE: 05-JUN-1995  
; APPLICATION NUMBER: PCT/US95/01780  
; FILING DATE: 08-FEB-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: STEFFE, ERIC K.  
; REGISTRATION NUMBER: 36,688  
; REFERENCE/DOCKET NUMBER: 1488.0380006  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)371-2600  
; TELEFAX: (202)371-2540  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 109 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-09-635-899-4

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Db 61 PRKEIIVWKNKNSIVCVDPOAEWIOQMMEVLKRKSSSTLPVPVFKRKIP 109  
RESULT 10  
US-09-588-044-2  
; Sequence 2, Application US/09588044  
; Patent No. 6692920  
; GENERAL INFORMATION:  
; APPLICANT: Guegler, Karl J.  
; Hawkins, Phillip R.  
; Wilde, Craig G.  
; Seilhamer, Jeffrey J.  
; TITLE OF INVENTION: A NOVEL CHEMOKINE EXPRESSED IN  
; INFLAMED ADENOID, ITS PRODUCTION AND USES  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: US  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/588,044  
; FILING DATE: 05-Jun-2000  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/352,324  
; FILING DATE: 07-DEC-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Luther, Barbara J.  
; REGISTRATION NUMBER: 33,954  
; REFERENCE/DOCKET NUMBER: PF-0025 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-855-0555  
; TELEFAX: 415-852-0195  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 109 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: polypeptide  
; IMMEDIATE SOURCE:  
; LIBRARY: Inflamed Adenoid  
; CLONE: 20293  
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-09-588-044-2

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Best Local Similarity 100.0%; Pred. No. 6e-98;  
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RESULT 11  
US-09-588-044-9  
; Sequence 9, Application US/09588044  
; Patent No. 6692920  
; GENERAL INFORMATION:  
; APPLICANT: Guegler, Karl J.

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;
;
;   Hawkins, Phillip R.
;   Wilde, Craig G.
;   Seilhamer, Jeffrey J.
;   TITLE OF INVENTION: A NOVEL CHEMOKINE EXPRESSED IN
;   INFLAMED ADENOID, ITS PRODUCTION AND USES
;
;   NUMBER OF SEQUENCES: 9
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Incyte Pharmaceuticals, Inc.
;   STREET: 3174 Porter Drive
;   CITY: Palo Alto
;   STATE: CA
;   COUNTRY: US
;   ZIP: 94304
;   MEDIUM TYPE: Diskette
;   COMPUTER: IBM compatible
;   OPERATING SYSTEM: DOS
;   SOFTWARE: FastSeq Version 1.5
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/588,044
;   FILING DATE: 05-Jun-2000
;   CLASSIFICATION: <Unknown>
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/352,324
;   FILING DATE: 07-DEC-1994
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Luther, Barbara J.
;   REGISTRATION NUMBER: 33,954
;   REFERENCE/DOCKET NUMBER: PF-0025 US
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 415-855-0555
;   TELEFAX: 415-852-0195
;   INFORMATION FOR SEQ ID NO: 9:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 109 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: peptide
;   SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-588-044-9

Query Match      100.0%; Score 109; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 6e-98;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKFISTLLMLLVSSLPVQGVLEVYVTSLRRCVQESSVFIPRRFIDRIQLPRGNGC 60
    |||||
Db 1 MKFISTLLMLLVSSLPVQGVLEVYVTSLRRCVQESSVFIPRRFIDRIQLPRGNGC 60
    |||||

QY 61 PRKEIIVWKKNSIVCVDPOAEWIQRMMEVLRKRSSTLPVPVFKRKIP 109
    |||||
Db 61 PRKEIIVWKKNSIVCVDPOAEWIQRMMEVLRKRSSTLPVPVFKRKIP 109
    |||||

RESULT 12
PCT-US95-01780-4
; Sequence 4, Application PC/TUS9501780
; GENERAL INFORMATION:
; APPLICANT: LI, ET AL.
; TITLE OF INVENTION: Human Chemokine Beta-11 and Human Chemokine Alpha-1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELIA, BYRNE, BAIN, GILFILLAN,
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2

Query Match      100.0%; Score 109; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 6e-98;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKFISTLLMLLVSSLPVQGVLEVYVTSLRRCVQESSVFIPRRFIDRIQLPRGNGC 60
    |||||
Db 1 MKFISTLLMLLVSSLPVQGVLEVYVTSLRRCVQESSVFIPRRFIDRIQLPRGNGC 60
    |||||

QY 61 PRKEIIVWKKNSIVCVDPOAEWIQRMMEVLRKRSSTLPVPVFKRKIP 109
    |||||
Db 61 PRKEIIVWKKNSIVCVDPOAEWIQRMMEVLRKRSSTLPVPVFKRKIP 109
    |||||

RESULT 13
PCT-US95-16144-2
; Sequence 2, Application PC/TUS9516144
; GENERAL INFORMATION:
; APPLICANT: INCYTE PHARMACEUTICALS, INC.
; TITLE OF INVENTION: A NOVEL CHEMOKINE EXPRESSED IN INFLAMED
; TITLE OF INVENTION: ADENOID, ITS PRODUCTION AND USES
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/16144
; FILING DATE: 07-DEC-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/352,324
; FILING DATE: 07-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: LUTHER, BARBARA J.
; REGISTRATION NUMBER: 33954
; REFERENCE/DOCKET NUMBER: PF-0025 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-852-0195
; INFORMATION FOR SEQ ID NO: 2:
;
;   OPERATING SYSTEM: MS-DOS
;   SOFTWARE: WORD PERFECT 5.1
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: PCT/US95/01780
;   FILING DATE: Concurrently
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:
;   FILING DATE:
;   ATTORNEY/AGENT INFORMATION:
;   NAME: FERRARO, GREGORY D.
;   REGISTRATION NUMBER: 36,134
;   REFERENCE/DOCKET NUMBER: 325800-272
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 201-994-1700
;   TELEFAX: 201-994-1744
;   INFORMATION FOR SEQ ID NO: 4:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 109 AMINO ACIDS
;   TYPE: AMINO ACID
;   STRANDEDNESS:
;   TOPOLOGY: LINEAR
;   MOLECULE TYPE: PROTEIN
;   PCT-US95-01780-4

Query Match      100.0%; Score 109; DB 5; Length 109;
Best Local Similarity 100.0%; Pred. No. 6e-98;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKFISTLLMLLVSSLPVQGVLEVYVTSLRRCVQESSVFIPRRFIDRIQLPRGNGC 60
    |||||
Db 1 MKFISTLLMLLVSSLPVQGVLEVYVTSLRRCVQESSVFIPRRFIDRIQLPRGNGC 60
    |||||

QY 61 PRKEIIVWKKNSIVCVDPOAEWIQRMMEVLRKRSSTLPVPVFKRKIP 109
    |||||
Db 61 PRKEIIVWKKNSIVCVDPOAEWIQRMMEVLRKRSSTLPVPVFKRKIP 109
    |||||
```

SEQUENCE CHARACTERISTICS:  
LENGTH: 109 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: polypeptide  
IMMEDIATE SOURCE:  
LIBRARY: Inflamed Adenoid  
CLONE: 20293  
PCT-US95-16144-2

Query Match 100.0%; Score 109; DB 5; Length 109;  
Best Local Similarity 100.0%; Pred. No. 6e-98;  
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MKFISTLLMLVSSLSPVQGVLEVYVYTSLRRCVQESSVFIPIRRFDRIQILPRGNGC 60  
DB 1 MKFISTLLMLVSSLSPVQGVLEVYVYTSLRRCVQESSVFIPIRRFDRIQILPRGNGC 60  
QY 61 PRKEIIVWKNKSIKVCVDPQAEWIORQMEVLKRKSSSTLPVPVFKRKIP 109  
DB 61 PRKEIIVWKNKSIKVCVDPQAEWIORQMEVLKRKSSSTLPVPVFKRKIP 109

RESULT 14  
PCT-US95-16144-9  
Sequence 9, Application PC/TUS9516144  
GENERAL INFORMATION:  
APPLICANT: INCYTE PHARMACEUTICALS, INC.  
TITLE OF INVENTION: A NOVEL CHEMOKINE EXPRESSED IN INFLAMED  
TITLE OF INVENTION: ADENOID, ITS PRODUCTION AND USES  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESS: INCYTE PHARMACEUTICALS, INC.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WordPerfect 6.1/MS-DOS 6.2  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/16144  
FILING DATE: 07-DEC-1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/352,324  
FILING DATE: 07-DEC-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: LUTHER, BARBARA J.  
REGISTRATION NUMBER: 33954  
REFERENCE/DOCKET NUMBER: PF-0025 PCT  
TELEPHONE: 415-855-0555  
TELEFAX: 415-852-0195  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 109 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US95-16144-9

Query Match 100.0%; Score 109; DB 5; Length 109;  
Best Local Similarity 100.0%; Pred. No. 6e-98;  
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MKFISTLLMLVSSLSPVQGVLEVYVYTSLRRCVQESSVFIPIRRFDRIQILPRGNGC 60

DB 1 MKFISTLLMLVSSLSPVQGVLEVYVYTSLRRCVQESSVFIPIRRFDRIQILPRGNGC 60  
QY 61 PRKEIIVWKNKSIKVCVDPQAEWIORQMEVLKRKSSSTLPVPVFKRKIP 109  
DB 61 PRKEIIVWKNKSIKVCVDPQAEWIORQMEVLKRKSSSTLPVPVFKRKIP 109  
RESULT 15  
US-09-949-016-7722  
Sequence 7722, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CLO01307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 7722  
LENGTH: 115  
TYPE: PRT  
ORGANISM: Human  
US-09-949-016-7722  
Query Match 100.0%; Score 109; DB 4; Length 115;  
Best Local Similarity 100.0%; Pred. No. 6.3e-98;  
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MKFISTLLMLVSSLSPVQGVLEVYVYTSLRRCVQESSVFIPIRRFDRIQILPRGNGC 60  
DB 7 MKFISTLLMLVSSLSPVQGVLEVYVYTSLRRCVQESSVFIPIRRFDRIQILPRGNGC 66  
QY 61 PRKEIIVWKNKSIKVCVDPQAEWIORQMEVLKRKSSSTLPVPVFKRKIP 109  
DB 67 PRKEIIVWKNKSIKVCVDPQAEWIORQMEVLKRKSSSTLPVPVFKRKIP 115  
Search completed: September 21, 2005, 13:50:03  
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